

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended): A method for determining a chemotherapeutic regimen for treating a ~~metastie~~ metastatic tumor in an individual having a primary and metastatic tumor, comprising
 - a) obtaining a primary tumor specimen;
 - b) determining expression levels of Thymidylate Synthase (TS) ~~EGFR~~ in a primary tumor comprising
 - 1) determining mRNA levels of TS ~~EGFR~~ in the primary tumor sample; and
 - 2) comparing the amount of TS ~~EGFR~~ mRNA levels in the primary tumor sample from step 1) to an amount of mRNA of an internal control gene; and
 - c) determining a chemotherapeutic regimen for treating the metastatic ~~metastie~~ tumor in the individual based on the amount of TS ~~EGFR~~ mRNA in the primary tumor sample and a predetermined threshold level for the TS ~~EGFR~~.
- 2- 4. (canceled)
5. (currently amended) The method of claim 1 wherein determining expression levels of TS ~~EGFR~~ comprises a fluorescence based real-time detection method.
- 6-16. (canceled)
17. (currently amended): A method for determining a chemotherapeutic regimen for treating a metastatic ~~metastie~~ tumor in an individual having a primary and metastatic tumor, comprising
 - a) obtaining a primary tumor specimen and fixing the specimen to obtain a fixed tumor specimen;
 - b) determining a gene expression level for TS ~~EGFR~~ in the fixed primary tumor specimen, comprising
 - 1) isolating mRNA for TS ~~EGFR~~ from the fixed tumor specimen, wherein the fixed tumor sample is heated in the presence of an effective amount of a chaotrophic agent and wherein the heating occurs at a temperature from about 50°C to about 100°C;

- 2) subjecting the mRNA to amplification using a pair of oligonucleotide primers capable of amplifying a region of TS-EGFR to obtain an amplified sample; and
- 3) determining the amount of TS-EGFR mRNA in the amplified sample;
- c) comparing the amount of TS-EGFR mRNA from step 3) to an amount of mRNA of an internal control gene; and
- d) determining a chemotherapeutic regimen for treating the metastatic ~~metastie~~ tumor in the individual based on the amount of TS-EGFR mRNA in the primary tumor sample and a predetermined threshold level for TS-EGFR.

18-19. (canceled)

20. (currently amended): The method of claim 17 wherein determining expression levels of TS-EGFR comprises a fluorescence based real-time detection method.

21-23. (canceled)

24. (currently amended): A method for determining a chemotherapeutic regimen for treating a metastatic ~~metastie~~ tumor in an individual having a primary and metastatic tumor, comprising

- a) obtaining a primary tumor specimen;
- b) fixing and paraffin embedding (FPE) the primary tumor specimen;
- c) deparaffinizing the tumor specimen to obtain a deparaffinized sample;
- d) determining gene expression levels for TS EGFR in the deparaffinized sample of the primary tumor specimen, comprising
 - 1) isolating TS EGFR mRNA from the deparaffinized sample, wherein said sample is heated to a temperature in the range of about 50°C to about 100°C; and
 - 2) determining the amount of TS EGFR mRNA by amplifying the mRNA using a pair of oligonucleotide primers capable of amplifying a region of EGFR to obtain an amplified sample;
- e) comparing the amount of TS-EGFR mRNA from step d) to an amount of mRNA of an internal control gene; and
- f) determining a chemotherapeutic regimen for treating the metastatic tumor in the individual based on the amount of TS EGFR mRNA in the amplified sample and a predetermined threshold level for TS EGFR.

25. (currently amended): A method for determining a chemotherapeutic regimen for treating a metastatic ~~metastatic~~ tumor in an individual having a primary and metastatic tumor, comprising
- a) obtaining a primary tumor specimen;
 - b) fixing and paraffin embedding (FPE) the primary tumor specimen;
 - c) deparaffinizing the tumor specimen to obtain a deparaffinized sample;
 - d) determining gene expression levels for TS-EGFR in the primary tumor specimen, comprising
 - 1) isolating mRNA from the deparaffinized sample, wherein said sample is heated to a temperature in the range of about 50°C to about 100°C; and
 - 2) determining the amount of TS-EGFR mRNA by amplifying the mRNA using an oligonucleotide primer pair, the pair comprising a primer having SEQ ID: ~~4~~ 7, or an oligonucleotide primer at least 80% identical therewith and hybridizes to a complement of SEQ ID NO: ~~4~~ 7 under stringent conditions; wherein said oligonucleotide is capable of amplifying a portion of the 5' untranslated region and Exon 1 of TS-EGFR mRNA isolated from fixed and paraffin embedded (FPE) tissue when used with SEQ ID NO: ~~2~~ 8, and a primer having SEQ ID: ~~2~~ 8 or an oligonucleotide primer at least 80% identical therewith and hybridizes to a complement of SEQ ID NO: ~~2~~ 8 under stringent conditions; and wherein said oligonucleotide primer is capable of amplifying a portion of the 5' untranslated region and Exon 1 of TS-EGFR mRNA isolated from fixed and paraffin embedded (FPE) tissue when used with SEQ ID NO: ~~4~~ 7
 - e) comparing the amount of TS-EGFR mRNA from step d) to an amount of mRNA of an internal control gene; and
 - f) determining a chemotherapeutic regimen for treating the metastatic ~~metastatic~~ tumor in the individual based on the amount of TS-EGFR mRNA in the amplified sample and a predetermined threshold level for the TS-EGFR.
26. (canceled).
27. (previously presented): The method of claim 20, 24, or 25 wherein the heating occurs at a temperature from about 75°C to about 100°C for a period of about 5 to about 120 minutes.